

Please replace the paragraph at page 29, lines 11-16 with the following:

D3 H-CDR1 of CC49 and 21/28'CL differ at three positions, 31, 32, and 34. The residue at position 31 is directly involved in ligand binding in 12 of the 31 complexes; in five of those, only main chain atoms were involved. The residue at position 32 is ligand contacting in eight of the 31 complexes of known structure. The residue at position 34 is involved in ligand contact in none of the 31 complexes of known structure. Residues at positions 32 and 34 of the CC49 H-CDR1 were replaced with the corresponding residues of 21/28'CL MAb (<sup>32,34</sup>H) to test whether positions 32 is important for ligand contact and in eliciting anti-idiotypic response.

Please replace the paragraph at page 30, lines 7-8 with the following:

D4 Variant <sup>32,34</sup>H: residues at positions 32 and 34 of the CC49 H-CDR1 were replaced with the corresponding residues of 21/28'CL MAb.

Please replace the paragraph at page 30, lines 9-10 with the following:

D5 Variant <sup>60-62, 64</sup>H: residues at positions 60, 61, 62 and 64 of the CC49 H-CDR2 were replaced with the corresponding residues of 21/28'CL MAb.

Please replace the sequence listing as follows:

Please enter the enclosed replacement sequence listing to replace the existing sequence listing in the subject application.